

FIG. 1A

-320
 CACTCGTCTGCCCTGGACTCCCGTCTCCTCCTGTCTCCGGCTTCCAGAGCTCCCTCC
 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 GTGAGCAGACGGGGACCTGAGGGCAGAGGACACAGGAGGCCCAAGGGTCTCGAGGGAGG
 -260 -240 -220
 TTATGGCAGCAGCTTCCCGGTCTCCGGCGCAGTTCTCAGCGACGACCCCTCTCGGTCCG
 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 AATACCGTCTCGAAGGGCGCAGAGGCCCGCTCAAGAGTCGCTGCTGGGAGAGCGAGGC
 -200 -180 -160
 GGGCTGAGCCAGTCCCTGGATGTTGCTGAACCTCTCGAGATCATGCCGGGGTTTGCTG
 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 CCCGACTCGGGTCAGGGACCTACAACGACTTTGAGAGCTCTAGTACGGCCCCCAACCGAC
 -140 -120 -100
 CTGCTTCCCCCGGGTGCCCACTGCCACCGCCCGCCCTCTGCTGCCGCCGTCCGGGGA
 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 GACGAAGGGCGGCCACGGTGACGGTGCGCGCGGGGAGACGACGGCGGCAGGGGCCCT
 -80 -60 -40
 TGCTCAGTAGCCCGCTGCCCGGCCCGCGATCCTGTCTCCTCGAAGCCGTTTGCTGC
 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 ACGAGTCATCGGGCGACGGCCCGGGCGCTAGGACACAAAGGAGCCCTTCGGCAACGACG
 -20 0 20
 MATCH WITH FIG. 1B

FIG. 1B

MATCH WITH FIG. 1A

TGCAGAGTTGCACGAAC TAGTCATGTTGCTGTGGAGTCCCGGCAGTGCACGAGCTG
 +-----+-----+-----+-----+-----+-----+-----+-----+
 ACGTCTCAACGTTGATCAGTACCAACGACACCCCTCAGGGGCGCCGTCACGTCGTCGAC
 : M V L W E S P R Q C S S W
 40 : 60 80

GACAC TTTGCGAGGGCTTTTGGCTGGCTGCTGCTGCTGCCCGTCATGCTACTCATCGTAGC
 CTGTGAAACGCTCCCGAAAACGACCGACGACGACGGCGCAGTACGATGAGTAGCATCG
 T L C E G F C W L L L L L P V M L L I V A
 100 120 140

CGGCCGGTGAA GCTCGCTGCTTCCCTACCTCCTTAAGTACTGCCAAACGCCCAACCGG
 +-----+-----+-----+-----+-----+-----+-----+-----+
 GCGGGCCACTTCGAGCGACGAAAGGATGGAGGAAATCACTGACGGTTTGCGGGTGGCC
R P V K L A A F P T S L S D C Q T P T G
 160 180 200

CTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACAC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
GACCTTAACGAGACCAATACTACTGTCTCTTTTACTAGAGAAAGGAGACACTGTGGTTGTG
W N C S G Y D D R E N D L F L C D T N T
220 240 260

CTGTAAATTGATCGGGAATGTTTAAGAAATTGGAGACACTGTGACTTGGCTCTGTCAGTTT
MATCH WITH FIG. 1C

MATCH WITH FIG. 1C

FIG. 1C

280	300	320
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340	360	380
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400	420	440
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460 480 500

MATCH WITH FIG. 1 D

FIG. 1D

MATCH WITH FIG. 1C

T S Q K E T S T C D I C Q F G A E C D E
520 540 560

AGATGCCGAGGATGTCTGGTGTGTGTAATATGACTGTCTCAAAACCAACTTCAATCC

TCTACGGCTCCTACAGACCCACACACATTTATAACTGACAAGAGTTGGTTGAAGTTAGG

D A E D V W C V C N I D C S Q T N F N P
580 600 620

CCTCTGCGCTTCTGATGGGAAATCTTTATGATAATGCATGCCAAATCAAGAAGCATCGTG

GGAGACGGGAAGACTACCCCTTTAGAAATACTATTACGTACGGTTTAGTTTCTTCGTAGCAC

L C A S D G K S Y D N A C Q I K E A S C
640 660 680

TCAGAAACAGGAGAAATTTGAAGTCATGTCTTTGGGTCGATGTCAAGATAACACAACACTAC

AGTCTTTGTCCCTCTTTAACTTCAGTACAGAAACCCAGCTACAGTTCTATTGTGTGATG

Q K Q E K I E V M S L G R C Q D N T T T
700 720 740

AACTACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCCAGAGAAATGCTAACAA

TTGATGATTCAGACTTCTACCCGTAATACGTTCTTGCTCTAATACGTCCTCTTACGATTGTT

T T K S E D G H Y A R T D Y A E N A N K
760 780 800

MATCH WITH FIG. 1E

FIG. 1E

MATCH WITH FIG. 1D

ATTAGAAAGTGCCAGAGAACACCACATACCTTGTCGGAACATTACAAATGGCTTCTG
 TAATCTTCTTTACCGGTCTCTTGTTGGTGTATGGAACAGGCCCTGTAATGTTACCGAAGAC
 L E S A R E H H I P C P E H Y N G F C
 820 840 860

CATGCATGGGAAGTGTAGCAATTCATCAATATGCAGGAGCCCATCTTGCAGGTGTGATGC
 GTACGTACCCCTTCACACTCGTAAGATAGTTATACGTCCCTCGGTAGAACGTCACACTACG
 M H G K C E H S I N M Q E P S C R C D A
 880 900 920

TGGTTATACTGGACAACACTGTGTGAAAAAAGGACTACAGTGTCTTATACGTGTTCCCGG
 ACCAATATGACCTGTTGTGACACTTTTTCCTGATGTCACAAGATATGCAACAAGGGCC
 G Y T G Q H C E K K D Y S V L Y V V P G
 940 960 980

TCCTGTACGATTTCAGTATGTCTTAATCGCAGCTGTGATTGGAACAATTTCAGATTGCTGT
 AGGACATGCTAAAGTCATACAGAAATTAGCGTCGACACTAACCTTGTTAAGTCTAACGACA
 P V R F Q Y V L I A A V I G T I Q I A V
 1000 1020 1040

CATCTGTGTGGTGCTCCTCTGCATCACAAAGGAAATGCCCCAGAAAGCAACAGAATTTCACAG
 GTAGACACACCAGGAGACGTAGTGTTCCTTTACGGGGTCTTTCGTTGTCTTAAAGTGC

MATCH WITH FIG. 1F

MATCH WITH FIG. 1E

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I  C  V  V  V  L  C  I  T  R  K  C  P  R  S  N  R  I  H  R
1060      .      1080      1100
ACAGAGCAAAATACAGGCACTACAGTTCGGACAATACAACAAGAGCGTCCACGAGGTT
-+-----+-----+-----+-----+-----+-----+-----+-----+
TGCTTCGTTTATGTCCCGTGATGTCAAGCCCTGTTATGTTGTTCTCGCAGGTGCTCCAA
Q  K  Q  N  T  G  H  Y  S  S  D  N  T  T  R  A  S  T  R  L
1120      .      1140      1160
AATCTAAAGGGAGCATGTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATAC
-+-----+-----+-----+-----+-----+-----+-----+-----+
TTAGATTTCCCTCGTACAAAGTGTCAACCGACCTGATGGCTCTCGAACCTGATGTTTATG
I  *
1180      .      1200      1220
AGTATTATAGACAAAGAATAAGACAAGAGATCTACACATGTTGCCCTTGCAATTGTGGTA
-+-----+-----+-----+-----+-----+-----+-----+-----+
TCATAATATCTGTTTCTTATTCGTCTCTAGATGTGTACAAACGGAACGTAAACACCAT
1240      .      1260      1280
ATCTACACCAATGAAACATGTACTACAGCTATATTTTGATTATGTTATGATATATTTGAA
-+-----+-----+-----+-----+-----+-----+-----+-----+
TAGATGTGGTTACTTTTGTACATGATGTGCGATATAAACTAATACATACCTATATAAACTT
1300      .      1320      1340
ATAGTATACATGTCTTGATGTTTCTGTAAATGTAATAAACTATTTATATCACACAA
-+-----+-----+-----+-----+-----+-----+-----+-----+
TATCATATGTAAACAGAACTACAAAAAAGACATTACATTTATTGATAAATATAGTGTGTT
1360
AAAAA
-+-----+-----+-----+-----+-----+-----+-----+-----+
TTTTTTTTTTTTTTTT

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FIG. 1F

FIG. 2A

	M	V	-	-	-	X	X	X	C	S	S	-	-	-	-	-	-	-	A	X	X	L	L	L	L	X	X	A	L	G	Majority	
1	M	D	-	-	-	R	A	R	C	S	G	-	-	-	-	-	-	-	A	S	S	L	P	L	L	L	A	L	A	L	G	hBCp
1	M	V	-	-	-	-	-	-	-	P	S	-	-	-	-	-	-	-	A	G	Q	L	A	L	F	-	-	A	L	G	hTGFap	
1	M	V	L	W	E	S	P	R	Q	C	S	S	W	T	L	C	E	G	F	C	W	L	L	L	L	P	V	M	L	L	TGfa95.aa	
	I	V	-	-	-	-	-	-	-	-	-	-	-	L	X	X	C	Q	X	X	X	G	X	X	X	X	X	-	-	-	Majority	
23	L	V	-	-	-	-	-	-	-	-	-	-	I	L	H	C	V	V	A	D	G	N	S	T	R	S	-	-	-	-	hBCp	
15	I	V	-	-	-	-	-	-	-	-	-	-	L	A	A	C	Q	A	L	E	N	S	T	S	P	-	-	-	-	hTGFap		
31	I	V	A	R	P	V	K	L	A	A	F	P	T	S	L	S	D	C	Q	T	P	T	G	W	N	C	S	G	Y	D	TGfa95.aa	
	-	X	E	X	X	X	L	C	X	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Majority	
39	-	P	E	T	N	G	L	L	C	G	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hBCp	
30	-	-	-	-	-	-	-	-	L	S	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hTGFap	
61	D	R	E	N	D	L	F	L	C	D	T	N	T	C	K	F	D	G	E	C	L	R	I	G	D	T	V	T	C	V	TGfa95.aa	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Majority	
49	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hBCp	
34	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	hTGFap	

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A		FIG. 2B	
91	C Q F K C N N D Y V P V C G S N G E S Y Q N E C Y L R Q A A	TG Fa95.aa	
	- - - - - P E X X C A X - - - - -	Majority	
	130 140 150		
49	- - - - - P E N C A A - - - - -	hBCp	
34	- - - - - P P V A A V - - - - -	hTG Fap	
121	C K Q Q S E I L V S E G S C A T D A G S G S G D G V H E G	TG Fa95.aa	
	- - - - -	Majority	
	160 170 180		
56	- - - - -	hBCp	
41	- - - - -	hTG Fap	
151	S G E T S Q K E T S T C D I C Q F G A E C D E D A E D V W C	TG Fa95.aa	
	- - - - -	Majority	
	190 200 210		
56	- - - - -	hBCp	
41	- - - - -	hTG Fap	
181	V C N I D C S Q T N F N P L C A S D G K S Y D N A C Q I K E	TG Fa95.aa	
	- - - - - T T T X X X X X G	Majority	
	220 230 240		
MATCH WITH FIG. 2C			

MATCH WITH FIG. 2B

[illegible]

MATCH WITH FIG. 2D

MATCH WITH FIG. 2C

FIG. 2D

	X	X	I	X	X	C	V	X	X	X	C	C	X	-	X	R	K	X	C	X	R	X	X	X	X	X	X	E	Majority		
1134	L	V	I	G	V	C	T	-	-	-	C	C	H	P	L	R	R	R	R	K	K	-	-	-	-	K	E	E	hBCp		
1113	V	L	I	I	T	C	V	L	I	H	C	C	Q	-	V	R	K	H	C	E	W	C	R	A	L	I	C	R	H	E	hTGFap
3331	I	A	V	-	I	C	V	V	V	L	C	-	-	-	I	T	R	K	C	P	R	S	N	R	I	H	R	Q	K	Q	TGFa95.aa
	X	X	X	X	L	X	K	D	X	T	X	X	-	-	X	X	X	X	X	X	X	I	X							Majority	
157	E	M	E	T	L	G	K	D	I	T	P	I	N	E	D	I	E	E	T	N	I	A								hBCp	
142	K	P	S	A	L	L	K	G	R	T	A	C	-	-	-	C	H	S	E	T	V	V								hTGFap	
357	N	T	G	H	Y	S	S	D	N	T	T	-	-	-	R	A	S	T	R	L	I									TGFa95.aa	

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Decoration 'Decoration #1': Shade with solid residues that match the Consensus exactly.